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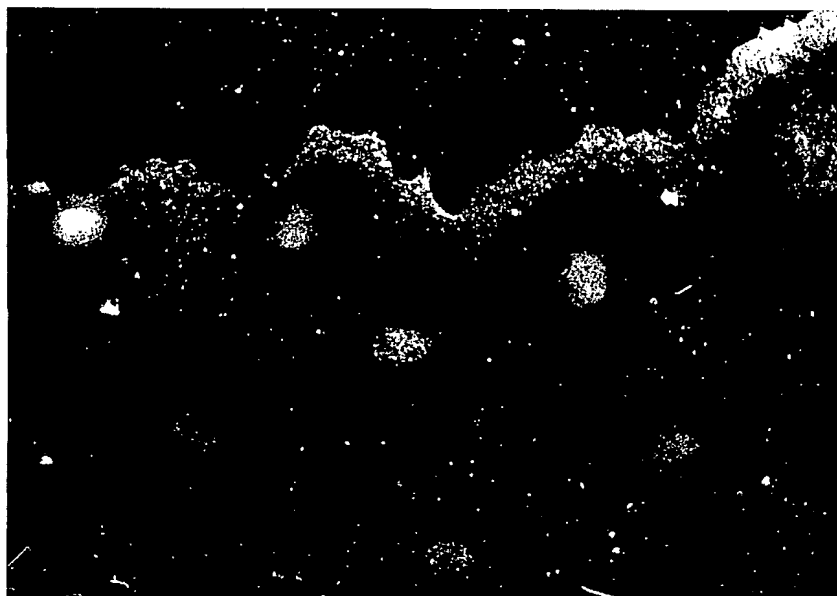


Fig. 1

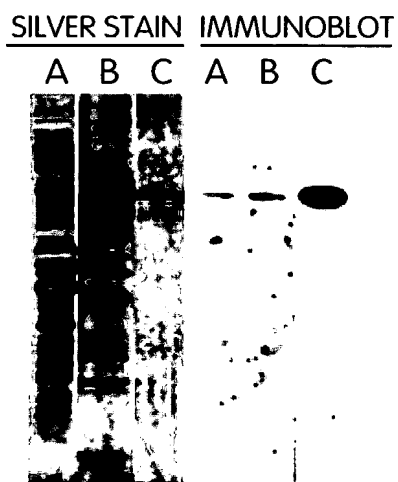


Fig. 2



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2/19

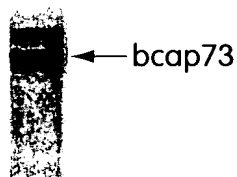


Fig. 3A

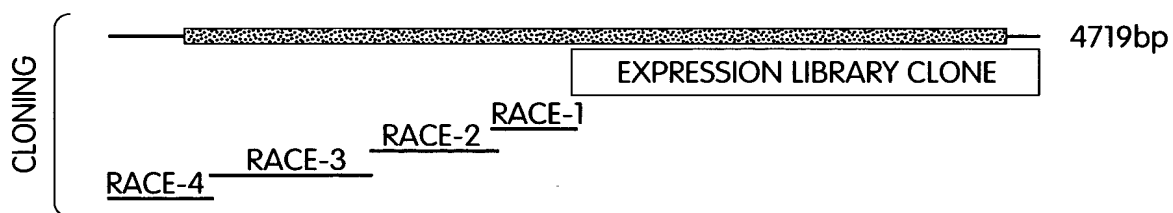


Fig. 3B

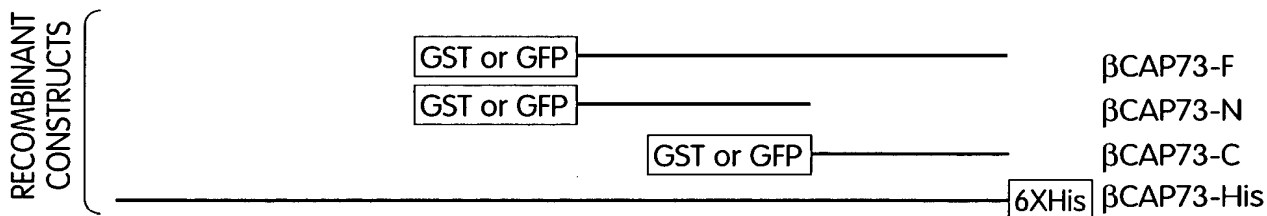


Fig. 3C



Fig. 3D



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3/19

cagtgttgag gcggcaggat gtagagtgt gttcaagctt tccagtggag tccccgaaaa 60
gggaaggcag agaaagacat cttctaaata acaaatagga ggagttacag tacctgactt 120
ggggctgctc ttaatcaagt gctgccgctg caaggaagat aattttcaag cgttatgaag 180
gcggagaagg attccgaaga cgaagaaaat atccttagag atccaagcta agtgtagtgc 240
agcatgaaga ttgcagaaca ggaagagttc taagaagaag gactgagtca ctagtttagga 300
gtctctctga gggctggctt tgtgagccac agtgatttgt aacttaatgc gaactaattt 360
gctgtagca acaagaaact aaatcctgtc t atg atg agc tgt tgg ttt tct 412
Met Met Ser Cys Trp Phe Ser
1 5

tgt gct cct aag aac aga caa gca gca gat tgg aac aaa tac gat gac 460
Cys Ala Pro Lys Asn Arg Gln Ala Ala Asp Trp Asn Lys Tyr Asp Asp
10 15 20

cga ttg atg aga gca gca gaa agg gga gat gta gaa aaa gtg tcc tca 508
Arg Leu Met Arg Ala Ala Glu Arg Gly Asp Val Glu Lys Val Ser Ser
25 30 35

atc ctt gct aaa aag gga gtc aat cca ggc aag cta gat gta gaa ggc 556
Ile Leu Ala Lys Lys Gly Val Asn Pro Gly Lys Leu Asp Val Glu Gly
40 45 50 55

aga tct gcc ttt cat gtt gtg gcc tca aag gga aat ctt gag tgt ttg 604
Arg Ser Ala Phe His Val Val Ala Ser Lys Gly Asn Leu Glu Cys Leu
60 65 70

aat gcc atc ctc ata cat gga gtt gat att aca acc agt gac acc gca 652
Asn Ala Ile Leu Ile His Gly Val Asp Ile Thr Thr Ser Asp Thr Ala
75 80 85

gga agg aat gct ctt cac ctg gct gca aag tat ggg cat gca ctg tgt 700
Gly Arg Asn Ala Leu His Leu Ala Ala Lys Tyr Gly His Ala Leu Cys
90 95 100

cta caa aaa ctt cta cag tac aat tgt ccc act gaa cat gta gac ctg 748
Leu Gln Lys Leu Leu Gln Tyr Asn Cys Pro Thr Glu His Val Asp Leu
105 110 115

cag gga aga act gca ctt cat gat gca gct atg gca gac tgt cct tct 796
Gln Gly Arg Thr Ala Leu His Asp Ala Ala Met Ala Asp Cys Pro Ser
120 125 130 135

agc ata cag ctg ctc tgc gac cat ggg gcc tcg gtg aat gcc aaa gat 844
Ser Ile Gln Leu Leu Cys Asp His Gly Ala Ser Val Asn Ala Lys Asp
140 145 150

Fig. 4-1



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4/19

gta gat ggg cgg aca cca ctt gtt ctg gct acc cag atg tgt agg cca	892
Val Asp Gly Arg Thr Pro Leu Val Leu Ala Thr Gln Met Cys Arg Pro	
155 160 165	
aca ata tgt caa ctg ctg ata gat aga ggg gcg gat att aat tcc aga	940
Thr Ile Cys Gln Leu Leu Ile Asp Arg Gly Ala Asp Ile Asn Ser Arg	
170 175 180	
gac aaa caa aac agg act gct ctc atg cta gga tgc gag tat ggt tgc	988
Asp Lys Gln Asn Arg Thr Ala Leu Met Leu Gly Cys Glu Tyr Gly Cys	
185 190 195	
aaa gat gca gta gaa gtc tta atc aaa aac ggc gct gac gtg acc ttg	1036
Lys Asp Ala Val Glu Val Leu Ile Lys Asn Gly Ala Asp Val Thr Leu	
200 205 210 215	
ctg gac gcc ctt ggc cat gac agt tct tac tat gca aga att ggt gac	1084
Leu Asp Ala Leu Gly His Asp Ser Ser Tyr Tyr Ala Arg Ile Gly Asp	
220 225 230	
aat ctg gac att cta acc tta ctg aag act gca tca gaa aat tcc aac	1132
Asn Leu Asp Ile Leu Thr Leu Leu Lys Thr Ala Ser Glu Asn Ser Asn	
235 240 245	
aaa ggg aga gaa ctt tgg aag aaa gga cca tct tta caa cag cga aat	1180
Lys Gly Arg Glu Leu Trp Lys Lys Gly Pro Ser Leu Gln Gln Arg Asn	
250 255 260	
ttg tct cag atg cta gat gaa gta aat acg aag tca aat cag agg gag	1228
Leu Ser Gln Met Leu Asp Glu Val Asn Thr Lys Ser Asn Gln Arg Glu	
265 270 275	
cat caa aac att cag gat ctg gag att gaa aat gaa gat ctg aaa gag	1276
His Gln Asn Ile Gln Asp Leu Glu Ile Glu Asn Glu Asp Leu Lys Glu	
280 285 290 295	
aga ttg aga aaa att cag caa gaa cag aga ata tta ttg gat aaa gtc	1324
Arg Leu Arg Lys Ile Gln Gln Glu Gln Arg Ile Leu Leu Asp Lys Val	
300 305 310	
aat ggt tta cag cta cag ctg aat gag gaa gta atg gtg gct gat gat	1372
Asn Gly Leu Gln Leu Gln Leu Asn Glu Glu Val Met Val Ala Asp Asp	
315 320 325	
ctg gaa agt gag aaa gaa aag ctg aag tcc ctt ttg gca gcc aaa gaa	1420
Leu Glu Ser Glu Lys Glu Lys Leu Lys Ser Leu Leu Ala Ala Lys Glu	
330 335 340	
aag cag cat gaa gaa agc cta aga act att gag gct ctg aaa agt aga	1468
Lys Gln His Glu Glu Ser Leu Arg Thr Ile Glu Ala Leu Lys Ser Arg	
345 350 355	

Fig. 4-2



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5/19

ttt aag tat ttt gag agt gat cat tta gga tca gga agt cat ttc agg	1516
Phe Lys Tyr Phe Glu Ser Asp His Leu Gly Ser Gly Ser His Phe Arg	
360 365 370 375	
aaa gaa gat atg ctt ctt aaa caa ggt caa atg tac atg aca gac tca	1564
Lys Glu Asp Met Leu Leu Lys Gln Gly Gln Met Tyr Met Thr Asp Ser	
380 385 390	
cag tgt act tcc aca ggc atg cca gtc cat atg caa agc cga tct atg	1612
Gln Cys Thr Ser Thr Gly Met Pro Val His Met Gln Ser Arg Ser Met	
395 400 405	
tta aga cca ctg gag cta gcc tta cct aat caa gcc tca tat tcg gaa	1660
Leu Arg Pro Leu Glu Leu Ala Leu Pro Asn Gln Ala Ser Tyr Ser Glu	
410 415 420	
aac gaa att tta aag aaa gaa tta gaa gca atg aga act ttc tgt gat	1708
Asn Glu Ile Leu Lys Lys Glu Leu Glu Ala Met Arg Thr Phe Cys Asp	
425 430 435	
tca gca aaa caa gac aga ctc aaa ctc caa aat gaa ctg gct cac aag	1756
Ser Ala Lys Gln Asp Arg Leu Lys Leu Gln Asn Glu Leu Ala His Lys	
440 445 450 455	
gtg gcg gag tgc aag gcc tta gca ttg gaa tgt gaa agg gtg aaa gag	1804
Val Ala Glu Cys Lys Ala Leu Ala Leu Glu Cys Glu Arg Val Lys Glu	
460 465 470	
gat tca gat gag cag ata aag caa cta gaa gat gcc ttg aaa gac gtg	1852
Asp Ser Asp Glu Gln Ile Lys Gln Leu Glu Asp Ala Leu Lys Asp Val	
475 480 485	
cag aag aga atg tat gag tcg gaa ggt aaa gtg aaa caa atg cag aca	1900
Gln Lys Arg Met Tyr Glu Ser Glu Gly Lys Val Lys Gln Met Gln Thr	
490 495 500	
cat ttt ctt gcc ttg aaa gag cac ctg aca agt gat gcg gcc act ggg	1948
His Phe Leu Ala Leu Lys Glu His Leu Thr Ser Asp Ala Ala Thr Gly	
505 510 515	
aac cac agg ctg atg gag gaa ctg aag gat cag ttg aaa gac atg aaa	1996
Asn His Arg Leu Met Glu Glu Leu Lys Asp Gln Leu Lys Asp Met Lys	
520 525 530 535	
gtg aaa tac gaa ggt gcg tcc gca gaa gtg ggg aaa ttg aga aac caa	2044
Val Lys Tyr Glu Gly Ala Ser Ala Glu Val Gly Lys Leu Arg Asn Gln	
540 545 550	
atc aaa caa aat gaa atg tta gtt gaa gag ttt aag aga gat gag ggc	2092
Ile Lys Gln Asn Glu Met Leu Val Glu Glu Phe Lys Arg Asp Glu Gly	
555 560 565	

Fig. 4-3



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6/19

aag ctg atg gaa gag aat aag cga ctg cag aag gag ttg agc atg tgt	2140
Lys Leu Met Glu Glu Asn Lys Arg Leu Gln Lys Glu Leu Ser Met Cys	
570 575 580	
gaa ctg gag cga gag aag aga gga agg aag ctc act gag atg gaa ggc	2188
Glu Leu Glu Arg Glu Lys Arg Gly Arg Lys Leu Thr Glu Met Glu Gly	
585 590 595	
cag tta aag gac ttg tca gcc aag ctg gcc ctt tct att cca gca gag	2236
Gln Leu Lys Asp Leu Ser Ala Lys Leu Ala Leu Ser Ile Pro Ala Glu	
600 605 610 615	
aaa ttt gaa aac atg aag agc ttg tta tca aat gaa ctg aac gag aag	2284
Lys Phe Glu Asn Met Lys Ser Leu Leu Ser Asn Glu Leu Asn Glu Lys	
620 625 630	
gca aaa aaa tta ata gat gtg gaa aga gaa tat gaa aga tca ctt aat	2332
Ala Lys Lys Leu Ile Asp Val Glu Arg Glu Tyr Glu Arg Ser Leu Asn	
635 640 645	
gaa act aga cca tta aag aga gaa ctt gag aat ttg aag gcc aaa ctg	2380
Glu Thr Arg Pro Leu Lys Arg Glu Leu Glu Asn Leu Lys Ala Lys Leu	
650 655 660	
gct cag cac gtc aaa cca gag gaa cat gag cag ctc aag agc aga tta	2428
Ala Gln His Val Lys Pro Glu Glu His Glu Gln Leu Lys Ser Arg Leu	
665 670 675	
gag cag aag tca gga gaa ctt ggg aag agg atc act gag tta aca tcg	2476
Glu Gln Lys Ser Gly Glu Leu Gly Lys Arg Ile Thr Glu Leu Thr Ser	
680 685 690 695	
aaa aat cag acg tta caa aag gaa atc gaa aag gtc tgc ctg gat aat	2524
Lys Asn Gln Thr Leu Gln Lys Glu Ile Glu Lys Val Cys Leu Asp Asn	
700 705 710	
aag ctc ctt aca caa caa gta aat aac tta aca act gaa atg aaa aat	2572
Lys Leu Leu Thr Gln Gln Val Asn Asn Leu Thr Thr Glu Met Lys Asn	
715 720 725	
cat tac gtc cct tta aaa gta agt gaa gaa atg aaa aag tca cat gat	2620
His Tyr Val Pro Leu Lys Val Ser Glu Glu Met Lys Lys Ser His Asp	
730 735 740	
gta att gtt gat gat ttg aat aaa aag ctt tca gat gtg aca cac aaa	2668
Val Ile Val Asp Asp Leu Asn Lys Lys Leu Ser Asp Val Thr His Lys	
745 750 755	
tat aca gaa aag aag ttg gaa atg gag aag ttg ctt atg gaa aat gcc	2716
Tyr Thr Glu Lys Lys Leu Glu Met Glu Lys Leu Leu Met Glu Asn Ala	
760 765 770 775	

Fig. 4-4



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7/19

agt	tta	agt	aaa	aat	gtc	agc	cgc	ctg	gaa	act	gtg	ttc	ata	cct	ccc	2764
Ser	Leu	Ser	Lys	Asn	Val	Ser	Arg	Leu	Glu	Thr	Val	Phe	Ile	Pro	Pro	
				780					785					790		
gag	aga	cac	gaa	aaa	gaa	atg	atg	gct	ctg	aaa	tcc	aat	atc	act	gaa	2812
Glu	Arg	His	Glu	Lys	Glu	Met	Met	Ala	Leu	Lys	Ser	Asn	Ile	Thr	Glu	
			795					800					805			
ctt	aag	aag	cag	ctg	tct	gaa	ctt	aat	aaa	aaa	tgt	ggt	gaa	gac	caa	2860
Leu	Lys	Lys	Gln	Leu	Ser	Glu	Leu	Asn	Lys	Lys	Cys	Gly	Glu	Asp	Gln	
			810					815				820				
gag	aaa	ata	tat	tca	ctc	atg	tct	gaa	aac	aat	gat	ttg	aaa	aag	acc	2908
Glu	Lys	Ile	Tyr	Ser	Leu	Met	Ser	Glu	Asn	Asn	Asp	Leu	Lys	Lys	Thr	
	825					830					835					
atg	agt	cat	cag	tat	gtg	ccc	gtg	aaa	acc	cat	gaa	gag	att	aaa	act	2956
Met	Ser	His	Gln	Tyr	Val	Pro	Val	Lys	Thr	His	Glu	Glu	Ile	Lys	Thr	
	840				845					850					855	
gcc	ttg	agt	agc	aca	ttg	gat	aaa	acc	aat	aga	gaa	tta	gta	gat	gtg	3004
Ala	Leu	Ser	Ser	Thr	Leu	Asp	Lys	Thr	Asn	Arg	Glu	Leu	Val	Asp	Val	
				860					865					870		
aag	aag	aag	tgt	gaa	gat	ata	aat	caa	gaa	ttt	gtg	aaa	ata	aaa	gat	3052
Lys	Lys	Lys	Cys	Glu	Asp	Ile	Asn	Gln	Glu	Phe	Val	Lys	Ile	Lys	Asp	
			875					880					885			
gag	aac	gaa	ata	tta	aaa	aga	aat	ctg	gag	aac	act	cag	aac	caa	gta	3100
Glu	Asn	Glu	Ile	Leu	Lys	Arg	Asn	Leu	Glu	Asn	Thr	Gln	Asn	Gln	Val	
			890					895				900				
aaa	gct	gag	tac	atc	agc	cta	aga	gag	cat	gaa	gaa	aag	atg	agt	ggc	3148
Lys	Ala	Glu	Tyr	Ile	Ser	Leu	Arg	Glu	His	Glu	Glu	Lys	Met	Ser	Gly	
	905					910					915					
cta	agg	aag	agc	atg	aag	aag	gtc	cag	gac	aac	agc	gct	gaa	ata	ctg	3196
Leu	Arg	Lys	Ser	Met	Lys	Lys	Val	Gln	Asp	Asn	Ser	Ala	Glu	Ile	Leu	
	920				925					930					935	
gct	aag	tac	aaa	aaa	agc	cag	gag	gag	att	gtc	acc	ctg	cat	gag	gag	3244
Ala	Lys	Tyr	Lys	Lys	Ser	Gln	Glu	Glu	Ile	Val	Thr	Leu	His	Glu	Glu	
				940					945					950		
att	gca	gcc	cag	aag	aga	gaa	ctc	gac	acg	ata	cag	gaa	tgc	atc	aag	3292
Ile	Ala	Ala	Gln	Lys	Arg	Glu	Leu	Asp	Thr	Ile	Gln	Glu	Cys	Ile	Lys	
			955					960					965			
cta	aaa	tat	gct	ccg	atc	atc	agc	ttg	gaa	gag	tgt	gag	aga	aaa	ttt	3340
Leu	Lys	Tyr	Ala	Pro	Ile	Ile	Ser	Leu	Glu	Glu	Cys	Glu	Arg	Lys	Phe	
			970				975					980				

Fig. 4-5



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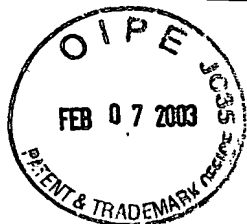
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8/19

aaa gcc act gag aaa gaa cta aaa gaa cag cta tcc cag cag aca cag	3388
Lys Ala Thr Glu Lys Glu Leu Lys Glu Gln Leu Ser Gln Gln Thr Gln	
985 990 995	
aag tat aat acc agt gaa gaa gag gcc aag aag tgc aag caa gag aat	3436
Lys Tyr Asn Thr Ser Glu Glu Glu Ala Lys Lys Cys Lys Gln Glu Asn	
1000 1005 1010 1015	
gac aag tta aag aag gag atc ctc act ctt cag aag gat cta aag gat	3484
Asp Lys Leu Lys Lys Glu Ile Leu Thr Leu Gln Lys Asp Leu Lys Asp	
1020 1025 1030	
aag aat gtt cac att gag aat tct tat gaa aca gaa aga gca tta agc	3532
Lys Asn Val His Ile Glu Asn Ser Tyr Glu Thr Glu Arg Ala Leu Ser	
1035 1040 1045	
aga aaa aca gaa gag ctg aac aga cag tta aaa gac ctg ttg cag aaa	3580
Arg Lys Thr Glu Glu Leu Asn Arg Gln Leu Lys Asp Leu Leu Gln Lys	
1050 1055 1060	
tac aca gag gca aag aag gag aaa gag aag ctc gtg gag gaa aat gcc	3628
Tyr Thr Glu Ala Lys Lys Glu Lys Glu Lys Leu Val Glu Glu Asn Ala	
1065 1070 1075	
aag cag act tct gag atc ctt gca gca caa act ctt ttg cag aag cag	3676
Lys Gln Thr Ser Glu Ile Leu Ala Ala Gln Thr Leu Leu Gln Lys Gln	
1080 1085 1090 1095	
cat gtt ccg ctg gag cag gtt gag tcc ctg aaa aaa tct ctt agt ggt	3724
His Val Pro Leu Glu Gln Val Glu Ser Leu Lys Lys Ser Leu Ser Gly	
1100 1105 1110	
aca atc gag aca ctc aag gaa gaa ctg aaa act aag cag aga tgt tat	3772
Thr Ile Glu Thr Leu Lys Glu Glu Leu Lys Thr Lys Gln Arg Cys Tyr	
1115 1120 1125	
gag aaa gag cag cag aca gtg acc caa ctg cgg cag atg ctg gag aat	3820
Glu Lys Glu Gln Gln Thr Val Thr Gln Leu Arg Gln Met Leu Glu Asn	
1130 1135 1140	
cag aag aac tcc tct gtg ccc ctg gct gag cat ttg cag gtt aag gaa	3868
Gln Lys Asn Ser Ser Val Pro Leu Ala Glu His Leu Gln Val Lys Glu	
1145 1150 1155	
gca ttt gag aaa gaa gtt gga atc ata aaa gct agc ttg aga gaa aag	3916
Ala Phe Glu Lys Glu Val Gly Ile Ile Lys Ala Ser Leu Arg Glu Lys	
1160 1165 1170 1175	
gaa gaa gaa agc caa aac aaa act gaa gag gtc tcc aaa ctc cag tct	3964
Glu Glu Glu Ser Gln Asn Lys Thr Glu Glu Val Ser Lys Leu Gln Ser	
1180 1185 1190	

Fig. 4-6



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gag att cag aat act aaa caa gcg tta aaa aaa tta gag act cgg gag	4012
Glu Ile Gln Asn Thr Lys Gln Ala Leu Lys Lys Leu Glu Thr Arg Glu	
1195 1200 1205	
gtg gtt gat ttg tcg aaa tat aaa gca acg aaa agc gat ttg gag aca	4060
Val Val Asp Leu Ser Lys Tyr Lys Ala Thr Lys Ser Asp Leu Glu Thr	
1210 1215 1220	
cag att tcc gac tta aac gaa aaa ttg gcc aat ctg aat agg aag tat	4108
Gln Ile Ser Asp Leu Asn Glu Lys Leu Ala Asn Leu Asn Arg Lys Tyr	
1225 1230 1235	
gag gaa gta tgt gag gag gtt ttg cat gcc aaa aag aag gaa ctg tct	4156
Glu Glu Val Cys Glu Glu Val Leu His Ala Lys Lys Lys Glu Leu Ser	
1240 1245 1250 1255	
gct aaa gat gag aag gaa ttg ctc cat ttc agc ata gag caa gaa atc	4204
Ala Lys Asp Glu Lys Glu Leu Leu His Phe Ser Ile Glu Gln Glu Ile	
1260 1265 1270	
aaa gat cag cag gaa cga tgt gac aaa tcc tta aca acc atc acg gag	4252
Lys Asp Gln Gln Glu Arg Cys Asp Lys Ser Leu Thr Thr Ile Thr Glu	
1275 1280 1285	
cta cag aga aga ata cag gaa tct gcc aaa caa atc gaa gca aaa gat	4300
Leu Gln Arg Arg Ile Gln Glu Ser Ala Lys Gln Ile Glu Ala Lys Asp	
1290 1295 1300	
aat aag ata act gaa ctg ctc aat gat gtg gag aga tta aaa cag gcc	4348
Asn Lys Ile Thr Glu Leu Leu Asn Asp Val Glu Arg Leu Lys Gln Ala	
1305 1310 1315	
ctc aat ggc ctt tcc cag ctc acc tat gga agt ggg agt ccc agc aag	4396
Leu Asn Gly Leu Ser Gln Leu Thr Tyr Gly Ser Gly Ser Pro Ser Lys	
1320 1325 1330 1335	
agg cag agt cag ctg att gac agc ctg cag cag cag gtc agg tcc ctg	4444
Arg Gln Ser Gln Leu Ile Asp Ser Leu Gln Gln Gln Val Arg Ser Leu	
1340 1345 1350	
cag cag cag ctg gcg gat gcc gac aga cag cac caa gaa gta att gca	4492
Gln Gln Gln Leu Ala Asp Ala Asp Arg Gln His Gln Glu Val Ile Ala	
1355 1360 1365	
att tat cgg aca cac ctt ctt agt gct gca cag ggt cac atg gat gag	4540
Ile Tyr Arg Thr His Leu Leu Ser Ala Ala Gln Gly His Met Asp Glu	
1370 1375 1380	
gat gtg cag gcc gcc tta ctg cag atc ata cag atg cgg cag ggg ctc	4588
Asp Val Gln Ala Ala Leu Leu Gln Ile Ile Gln Met Arg Gln Gly Leu	
1385 1390 1395	

Fig. 4-7



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gtg tgc tagtcggcac cccccagccc acagtggcctt tccctgctgg tgctgagcat 4644
Val Cys
1400
tctgtgcgca acttcatggc ctttctgggc ctgctgtgc tagtataatt aaaataaagt 4704
gtattttgat ccatcaaaaa aaaaaaaaaa aa 4736

Fig. 4-8



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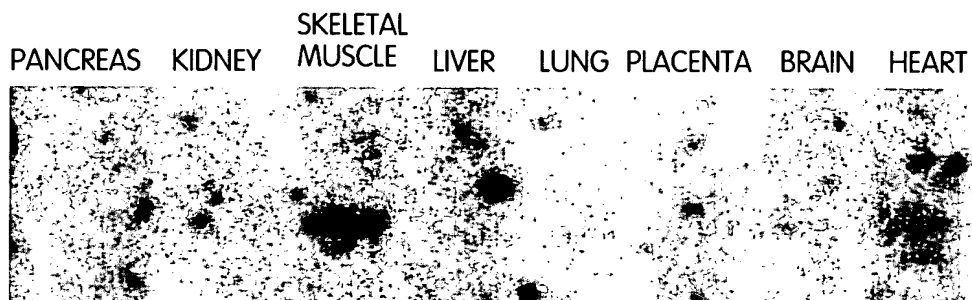


Fig. 5

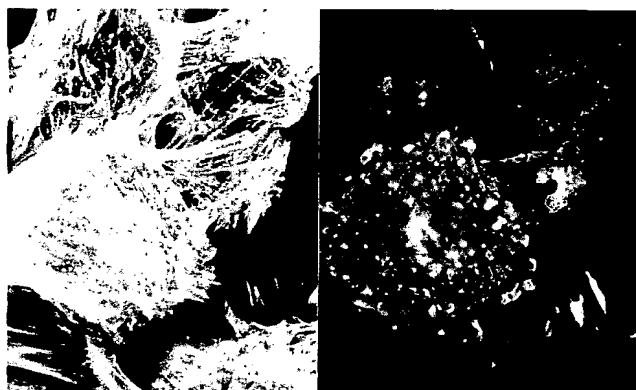


Fig. 6



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Fig. 7A

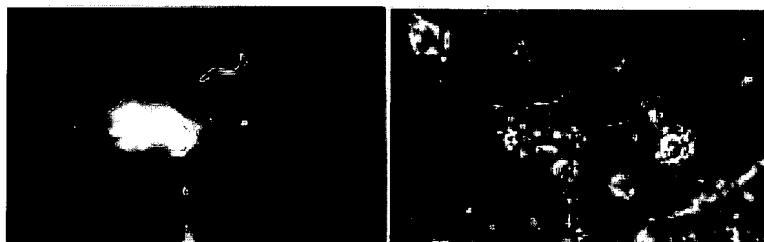


Fig. 7B

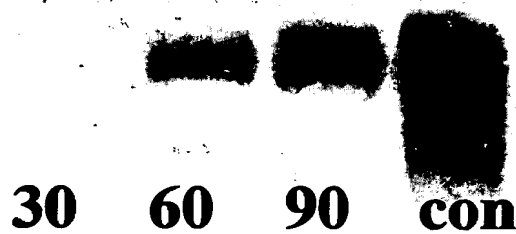


Fig. 8



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Sequence Alignment of bcap73 cDNA against Canine familiaris mRNA for C3VS protein
(GenBank accession X99145)

Query= β CAP73
Sbjct=C3VS

```
Query: 358  tttgctgtagcaacaagaaactaaatcctgtctatgatgagctgttggttttcttgtgc 417
           |||
Sbjct: 12   tttgctgtagcaaccagaaaccaaactcctgtctatgatgaactgttggttttcttgtgc 71

Query: 418  tcctaagaacagacaagcagcagattggaacaaatacgatgaccgattgatgagagcagc 477
           |||
Sbjct: 72   tcccaagaacagacatgcagcagattggaacaaatatgatgaccgattgatgaaagccgc 131

Query: 478  agaaaggggagatgtagaaaaagtgtcctcaatccttgctaaaaagggagtcfaatccagg 537
           |||
Sbjct: 132  ggagaggggagatgtagaaaaagttcctcaatccttgctaaaaagggcatfaatccagg 191

Query: 538  caagctagatgtagaaggcagatctgcctttcatgttggtggcctcaaagggaaatcttga 597
           |||
Sbjct: 192  caaactagatgtggaaggcagatctgccttccatgttggtggcctcaaaggggaatcttga 251

Query: 598  gtgtttgaatgccatcctcatacatggagttgatattacaaccagtgcaccgcaggaag 657
           |||
Sbjct: 252  atgtttgaatgccatccttatacatggagttgatattacaaccagtgcactgcaggaag 311

Query: 658  gaatgctcttcacctggctgcaaagtatgggcatgcactgtgtctacaaaaacttctaca 717
           |||
Sbjct: 312  aaatgctcttcacttggctgcaaagtatgggcatgcattgtgtctacaaaaacttctaca 371

Query: 718  gtacaattgtcccactgaacatgtagacctgcagggaagaactgcacttcatgatgcagc 777
           |||
Sbjct: 372  gtacaattgtcccactgaacatgcagacctgcagggaagaaccgcacttcatgcagcagc 431

Query: 778  tatggcagactgtccttctagcatacagctgctctgcgaccatggggcctcggatgaatgc 837
           |||
Sbjct: 432  aatggcagactgtccttccagcatacagctgcttctgtgaccatggggcctcggatgaatgc 491

Query: 838  caaagatgtagatgggaggacaccacttggttctggctaccagatgtgtaggccaacaat 897
           |||
Sbjct: 492  caaagatgtgatgggaggacaccgctggttctggctactcagatgtgtaggccagcaat 551
```

Fig. 9-1

TECH CENTER 1600/2900

15/19

Query: 1566 agtgtacttccacaggcatgccagtcctatgcaaagccgatctatgttaagaccactgg 1625

Sbjct: 1136 agtgtacttccccaggggtgccagcccacatgcaaagcaggtctatgttaagaccactgg 1195

Query: 1626 agctagccttacctaataagcctcatattcggaaaacgaaattttaagaaagaattag 1685

Sbjct: 1196 agctatcattaccaatcaaacctcatattctgaaaatgacctcttaaagaaagagttag 1255

Query: 1686 aagcaatgagaactttctgtgattcagcaaaacaagacagactcaaactccaaaatgaac 1745

Sbjct: 1256 aagcaatgagaactttctgcgaatcagccaaacaagaccgcctcaagctccagaacggag 1315

Query: 1746 **tggctcacaaggtggcggagtgcaaggccttagcattggaatgtgaaagggtgaaagagg** 1805

Sbjct: 1316 tggcgcacaaaggtggctgagtgcaaagctttaggactagaatgtgaacgcacaaaggagg 1375

Query: 1806 attcagatgagcagataaagcaactagaagatgccttgaaagacgtgcagaagagaatgt 1865

Sbjct: 1376 actctgatgagcagataaagcagttagaagacgcattgaaagatgtgcagaagagaatgt 1435

Query: 1866 atgagtcggaaggtaaagtgaacaaatgcagacacattttcttgccttgaaagagcacc 1925

Sbjct: 1436 atgagtcggaaggtaaagtaaaacaaatgcagacacacttttcttgcccttaaagagcacc 1495

Query: 1926 tgacaagtgatgctggccactgggaaccacaggctgatggaggaactgaaggatcagttga 1985

Sbjct: 1496 tgaccagtgaagcagctataggaatcacagactaatggaggagctgaaggatcagttga 1555

Query: 1986 aagacatgaaagtgaatacgaaggtgcgtccgcagaagtggggaaattgagaaaccaa 2045

Sbjct: 1556 aggacatgaaagcgaaatatgagggatgcatcagcagaagtgggaaaactgcgaaaccaa 1615

Query: 2046 tcaaacaaatgaaatgtagttgaagagtttaagagagatgagggcaagctgatggaag 2105

Sbjct: 1616 tcaaacaaaatgagctgctagtagaacagtttaggagagatgaaggcaagctggtggaag 1675

Query: 2106 agaataagcgactgcagaaggagttgagcatgtgtgaactggagcgagagaagagaggaa 2165

Sbjct: 1676 agaataagcgattgcagaaggaactcagtatgtgtgaaacggagcgagacaagaaaggaa 1735

Fig. 9-3



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16/19

Query: 2166 ggaagctcactgagatggaaggccagttaaaggacttgtcagccaagctggccctttcta 2225

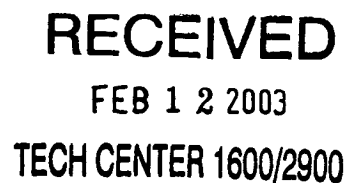
Sbjct: 1736 ggaggggttgctgaggtggaaggccaggtaaaggaactcttagcaaagctgaccttgtcag 1795

Query: 2226 ttccagcagagaaatttgaaaacatgaagagcttggttatcaa 2267

Sbjct: 1796 ttccaactgaaaaatttgagagcatgaagagcttattatcaa 1837

Fig. 9-4

Fig. 10-1



TECH CENTER 1600/2900

Sbjct: 486 tagaagaaaatgccaaacagacttctgagatacttgcaagtgcaaaatcttttgcaaaaac 545

Sbjct: 546 aacatgttccattggaacaggttgaggctctgaaaaaatctcttaatggcacaattgaaa 605

Sbjct: 606 atctaaaggaagaactgaagagtatgcaaaggtgttacgagaaagagcagcagacagtga 665

Sbjct: 666 ccaaactgcatcaattgttggagaatcaaaagaactcttctgtaccctggcagagcatt 725

Sbjct: 726 tgcagattaaagaagcatttgagaaagaagttggaatcataaaagccagcttgagagaaaa 785

Sbjct: 786 aggaagaagaaagccaaaacaaaatggaagaagtctccaaacttcagtcggaagttcaga 845

Sbjct: 846 atactaaacaagcmttaaaaaaattagagactagagaggtagttgacttqtctaaatata 905

Sbjct: 906 aagcaacaaaaagtgatttggagacacagatttctagcttaaattgaaaaattggccaatc 965

Sbjct: 966 tgaatagaaagtatgaggaagt-tgtgaggaagttttgcatgccmaaaagaaggaaatat 1024

Sbjct: 1025 ctgscaaagatgagaagga-ttactgc-tttcaccttgagscaggaaattaagggtcagr 1082

Fig. 10-2



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TECH CENTER 1600/2900

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Query: 4215 aggaacgatgtg 4226

Sbjct: 1083 aggaacgatgtg 1094

Fig. 10-3